

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/671,953B

CRF Processing Date: 11/17/2002  
 Edited by: [Signature]  
 Verified by: [Signature] (STIC staff)

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NOV 12 2002

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- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☒ Inserted mandatory headings, specifically: <2207 in sequences 17,21
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

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\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

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1600

RAW SEQUENCE LISTING

DATE: 11/07/2002

PATENT APPLICATION: US/09/671,953B

TIME: 20:55:42

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\11072002\I671953B.raw

P.6

```

3 <110> APPLICANT: Meares, Claude
4     Chmura, Albert
5     The Regents of the University of California
7 <120> TITLE OF INVENTION: Engineering Antibodies That Bind Irreversibly
9 <130> FILE REFERENCE: 023070-099120US
11 <140> CURRENT APPLICATION NUMBER: US 09/671,953B
12 <141> CURRENT FILING DATE: 2000-09-27
14 <150> PRIOR APPLICATION NUMBER: US 60/156,194
15 <151> PRIOR FILING DATE: 1999-09-27
17 <150> PRIOR APPLICATION NUMBER: US 60/208,684
18 <151> PRIOR FILING DATE: 2000-05-31
20 <160> NUMBER OF SEQ ID NOS: 23
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 753
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Description of Artificial Sequence:nucleic acid
31     that encodes Fab heavy chain of CHA255
33 <400> SEQUENCE: 1
34 agatctgaag tgacgtcgtt ggagtcctagg ggagactcag tgaagcctgg agggttcctg 60
35 aaactctcct gtgcagcctc tggattcact ttaagtgggt aaaccatgtc ttgggttcgc 120
36 cagactccgg agaagaggct ggagtggttc acaaccactc ttagtggtgg tggtttcacc 180
37 ttctattcag ccagtgtgaa gggtcgtttc accatctcca gagacaatgc ccagaacaac 240
38 ctctatctac aactgaatag tctgaggtct gaggacacgg ccttgatatt ctgtgcaagt 300
39 catcggtttg ttcactgggg ccacgggact ctggtcactg tctctgcagc caaaacgacg 360
40 ggcccatcgg tcttccccct ggcacctcc tccaagagca cctctggggg cacagcggcc 420
41 ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cgggtgcgtg gaactcaggc 480
42 gccctgacca gcggcggtgca caccttcccc gctgtcctac agtcctcaag actctacttc 540
43 ctgagcagcg tgggtgaccgt gcccttcaac agcttgggca ccagacctc catctgcaac 600
44 gtgaatcaca agcccagcaa caccaagggt gacaagaaag cagagcccaa atcttgtgac 660
45 aaatctagag ggcccttoga aggtaagcct atccctaacc ctctcctcgg tctcgattct 720
46 acgcgtaccg gtcacatca ccatcaccat tga 753
49 <210> SEQ ID NO: 2
50 <211> LENGTH: 657
51 <212> TYPE: DNA
52 <213> ORGANISM: Artificial Sequence
54 <220> FEATURE:
55 <223> OTHER INFORMATION: Description of Artificial Sequence:nucleic acid
56     that encodes light chain mutant with Cys
57     substituted for Asn at position 97 of CHA255
59 <400> SEQUENCE: 2

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Input Set : A:\PTO.AMC.txt

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60 agatctgctg ttgtgactca ggaatctgca ctcaccacat cacctgggtga aacagtcaca 60
61 ctcaacttgct gctcaagtat tggggctggt acaactagta actatgccaa ctgggtccaa 120
62 gaaaaaaccag atcatttatt cactgggtcta ataggtggta ccaataaccg ggctccgggt 180
63 gttcctgcca gattctcagg ctccctgatt ggagacaagg ctgccctcac catcacaggg 240
64 gcacagactg aagatgaggc aagatatttc tgtgctctat ggtactcctg cctctgggtr 300
65 ttcggtggag gaaccaaact gactgtccta agccgwackg tggctgcacc atctgtcttc 360
66 atcttcccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 420
67 aataacttct atcccagaga ggccaaagta cagtggaaagg tggataacgc cctccaatcg 480
68 ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 540
69 agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc 600
70 acccatcagg gcctgagyty gcccgtcaca aagagcttca acaggggaga gtgttaa 657
73 <210> SEQ ID NO: 3
74 <211> LENGTH: 657
75 <212> TYPE: DNA
76 <213> ORGANISM: Artificial Sequence
78 <220> FEATURE:
79 <223> OTHER INFORMATION: Description of Artificial Sequence:nucleic acid
80 that encodes the unmodified light chain of CHA255
82 <400> SEQUENCE: 3
83 agatctgctg ttgtgactca ggaatctgca ctcaccacat cacctgggtga aacagtcaca 60
84 ctcaacttgct gctcaagtat tggggctggt acaactagta actatgccaa ctgggtccaa 120
85 gaaaaaaccag atcatttatt cactgggtcta ataggtggta ccaataaccg ggctccgggt 180
86 gttcctgcca gattctcagg ctccctgatt ggagacaagg ctgccctcac catcacaggg 240
87 gcacagactg aagatgaggc aagatatttc tgtgctctat ggtactccaa cctctgggtr 300
88 ttcggtggag gaaccaaact gactgtccta agccgwackg tggctgcacc atctgtcttc 360
89 atcttcccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 420
90 aataacttct atcccagaga ggccaaagta cagtggaaagg tggataacgc cctccaatcg 480
91 ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 540
92 agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc 600
93 acccatcagg gcctgagyty gcccgtcaca aagagcttca acaggggaga gtgttaa 657
96 <210> SEQ ID NO: 4
97 <211> LENGTH: 657
98 <212> TYPE: DNA
99 <213> ORGANISM: Artificial Sequence
101 <220> FEATURE:
102 <223> OTHER INFORMATION: Description of Artificial Sequence:nucleic acid
103 that encodes light chain mutant with Cys
104 substituted for Ser at position 96 of CHA255
106 <400> SEQUENCE: 4
107 agatctgctg ttgtgactca ggaatctgca ctcaccacat cacctgggtga aacagtcaca 60
108 ctcaacttgct gctcaagtat tggggctggt acaactagta actatgccaa ctgggtccaa 120
109 gaaaaaaccag atcatttatt cactgggtcta ataggtggta ccaataaccg ggctccgggt 180
110 gttcctgcca gattctcagg ctccctgatt ggagacaagg ctgccctcac catcacaggg 240
111 gcacagactg aagatgaggc aagatatttc tgtgctctat ggtactgcaa cctctgggtr 300
112 ttcggtggag gaaccaaact gactgtccta agccgwackg tggctgcacc atctgtcttc 360
113 atcttcccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 420
114 aataacttct atcccagaga ggccaaagta cagtggaaagg tggataacgc cctccaatcg 480
115 ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 540
116 agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc 600

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117 acccatcagg gcctgagyty gcccgtcaca aagagcttca acaggggaga gtgttaa      657
120 <210> SEQ ID NO: 5
121 <211> LENGTH: 218
122 <212> TYPE: PRT
123 <213> ORGANISM: Artificial Sequence
125 <220> FEATURE:
126 <223> OTHER INFORMATION: Description of Artificial Sequence:polypeptide
127     sequence of mutant light chain with Cys
128     substituted for Asn at position 97 of CHA255
130 <220> FEATURE:
131 <221> NAME/KEY: MOD_RES
132 <222> LOCATION: (207)
133 <223> OTHER INFORMATION: Xaa = any amino acid
135 <400> SEQUENCE: 5
136 Arg Ser Ala Val Val Thr Gln Glu Ser Ala Leu Thr Thr Ser Pro Gly
137   1              5              10              15
139 Glu Thr Val Thr Leu Thr Cys Arg Ser Ser Ile Gly Ala Val Thr Thr
140           20              25              30
142 Ser Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr
143       35              40              45
145 Gly Leu Ile Gly Gly Thr Asn Asn Arg Ala Pro Gly Val Pro Ala Arg
146   50              55              60
148 Phe Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly
149  65              70              75              80
151 Ala Gln Thr Glu Asp Glu Ala Arg Tyr Phe Cys Ala Leu Trp Tyr Ser
152           85              90              95
154 Cys Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Arg
155       100              105              110
157 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
158       115              120              125
160 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
161       130              135              140
163 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
164 145              150              155              160
166 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
167           165              170              175
169 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
170       180              185              190
W--> 172 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Xaa Pro
173       195              200              205
175 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
176       210              215
179 <210> SEQ ID NO: 6
180 <211> LENGTH: 218
181 <212> TYPE: PRT
182 <213> ORGANISM: Artificial Sequence
184 <220> FEATURE:
185 <223> OTHER INFORMATION: Description of Artificial Sequence:polypeptide
186     sequence of unmodified light chain of CHA255

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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/671,953B

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Input Set : A:\PTO.AMC.txt  
 Output Set: N:\CRF4\11072002\I671953B.raw

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188 <220> FEATURE:
189 <221> NAME/KEY: MOD_RES
190 <222> LOCATION: (207)
191 <223> OTHER INFORMATION: Xaa = any amino acid
193 <400> SEQUENCE: 6
194 Arg Ser Ala Val Val Thr Gln Glu Ser Ala Leu Thr Thr Ser Pro Gly
195 1 5 10 15
197 Glu Thr Val Thr Leu Thr Cys Arg Ser Ile Gly Ala Val Thr Thr
198 20 25 30
200 Ser Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr
201 35 40 45
203 Gly Leu Ile Gly Gly Thr Asn Asn Arg Ala Pro Gly Val Pro Ala Arg
204 50 55 60
206 Phe Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly
207 65 70 75 80
209 Ala Gln Thr Glu Asp Glu Ala Arg Tyr Phe Cys Ala Leu Trp Tyr Ser
210 85 90 95
212 Asn Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Arg
213 100 105 110
215 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
216 115 120 125
218 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
219 130 135 140
221 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
222 145 150 155 160
224 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
225 165 170 175
227 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
228 180 185 190
W--> 230 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Xaa Pro
231 195 200 205
233 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
234 210 215
237 <210> SEQ ID NO: 7
238 <211> LENGTH: 218
239 <212> TYPE: PRT
240 <213> ORGANISM: Artificial Sequence
242 <220> FEATURE:
243 <223> OTHER INFORMATION: Description of Artificial Sequence: polypeptide
244 sequence of mutant light chain with Cys
245 substituted for Ser at position 96 of CHA255
247 <220> FEATURE:
248 <221> NAME/KEY: MOD_RES
249 <222> LOCATION: (207)
250 <223> OTHER INFORMATION: Xaa = any amino acid
252 <400> SEQUENCE: 7
253 Arg Ser Ala Val Val Thr Gln Glu Ser Ala Leu Thr Thr Ser Pro Gly
254 1 5 10 15
256 Glu Thr Val Thr Leu Thr Cys Arg Ser Ser Ile Gly Ala Val Thr Thr

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257          20          25          30
259 Ser Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr
260          35          40          45
262 Gly Leu Ile Gly Gly Thr Asn Asn Arg Ala Pro Gly Val Pro Ala Arg
263          50          55          60
265 Phe Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly
266          65          70          75          80
268 Ala Gln Thr Glu Asp Glu Ala Arg Tyr Phe Cys Ala Leu Trp Tyr Cys
269          85          90          95
271 Asn Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Arg
272          100          105          110
274 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
275          115          120          125
277 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
278          130          135          140
280 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
281          145          150          155          160
283 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
284          165          170          175
286 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
287          180          185          190
W--> 289 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Xaa Pro
290          195          200          205
292 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
293          210          215
296 <210> SEQ ID NO: 8
297 <211> LENGTH: 250
298 <212> TYPE: PRT
299 <213> ORGANISM: Artificial Sequence
301 <220> FEATURE:
302 <223> OTHER INFORMATION: Description of Artificial Sequence: polypeptide
303     sequence of unmodified heavy chain of CHA255
305 <400> SEQUENCE: 8
306 Arg Ser Glu Val Thr Leu Val Glu Ser Arg Gly Asp Ser Val Lys Pro
307     1          5          10          15
309 Gly Gly Phe Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser
310          20          25          30
312 Gly Glu Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu
313          35          40          45
315 Trp Val Thr Thr Thr Leu Ser Gly Gly Gly Phe Thr Phe Tyr Ser Ala
316          50          55          60
318 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Gln Asn Asn
319          65          70          75          80
321 Leu Tyr Leu Gln Leu Asn Ser Leu Arg Ser Glu Asp Thr Ala Leu Tyr
322          85          90          95
324 Phe Cys Ala Ser His Arg Phe Val His Trp Gly His Gly Thr Leu Val
325          100          105          110
327 Thr Val Ser Ala Ala Lys Thr Thr Gly Pro Ser Val Phe Pro Leu Ala
328          115          120          125

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/671,953B

DATE: 11/07/2002  
TIME: 20:55:43

Input Set : A:\PTO.AMC.txt  
Output Set: N:\CRF4\11072002\I671953B.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 207  
Seq#:6; Xaa Pos. 207  
Seq#:7; Xaa Pos. 207  
Seq#:20; N Pos. 405